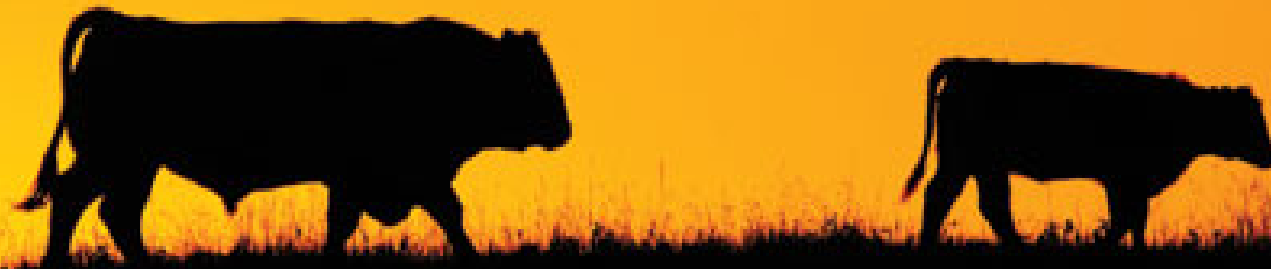


Crossbred Reference Can Improve Response To Genomic Selection

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EAAP 2014

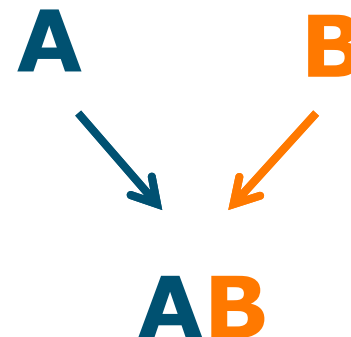


ACKNOWLEDGEMENTS



BACKGROUND

- Most of the animals used in livestock production systems are crossbreds
- Limitations
 - Selection is in purebred nucleus lines or breeds that are housed in high-health environments
 - Genetic differences



BACKGROUND

- Genomic selection

- Training on crossbreds
 - Collection of crossbred P and G
 - SNP effects might be breed specific

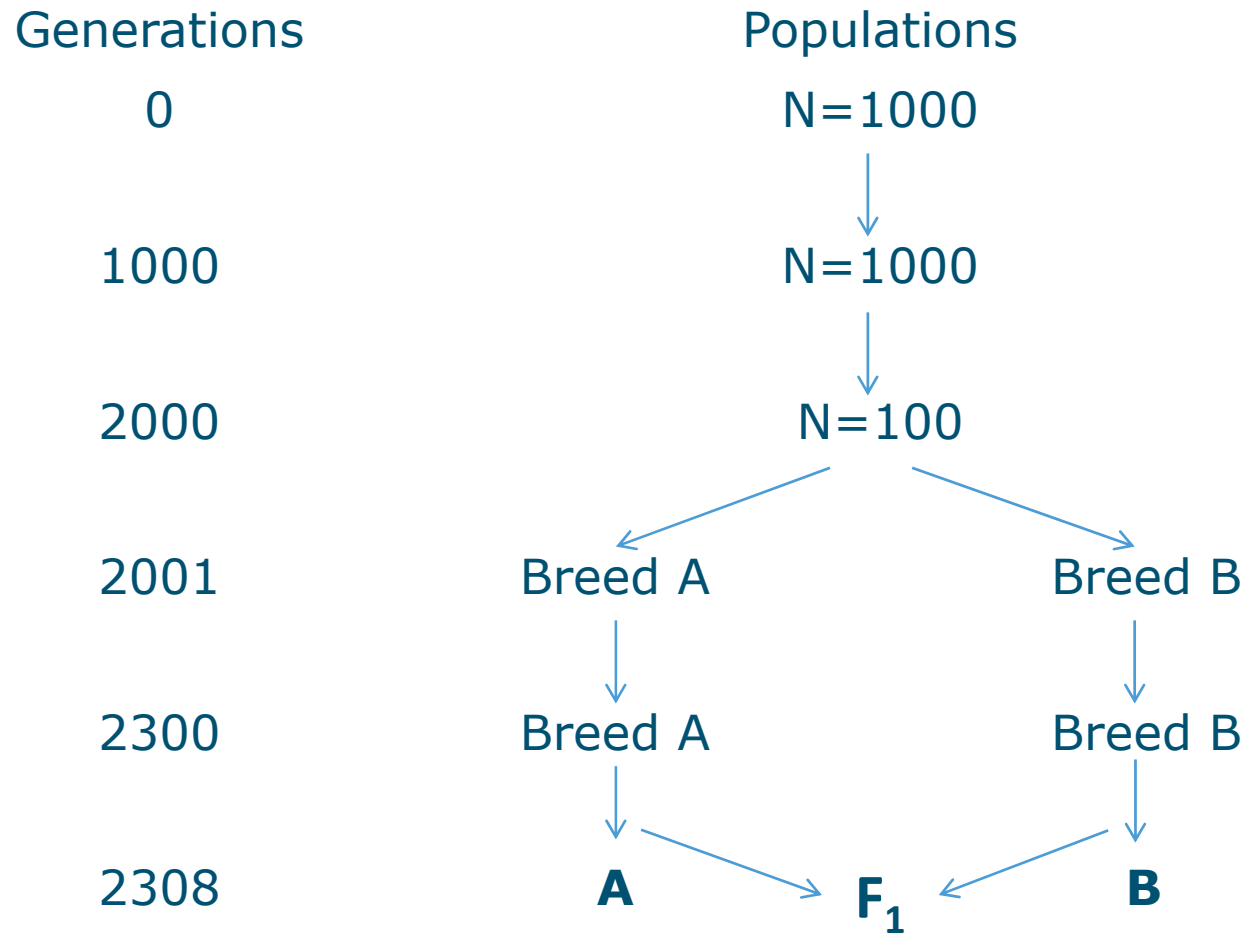
- Training on pure lines
 - Environmental differences between purebreds and crossbred animals
 - G×E

OBJECTIVE

- To compare crossbred response by variety of training populations

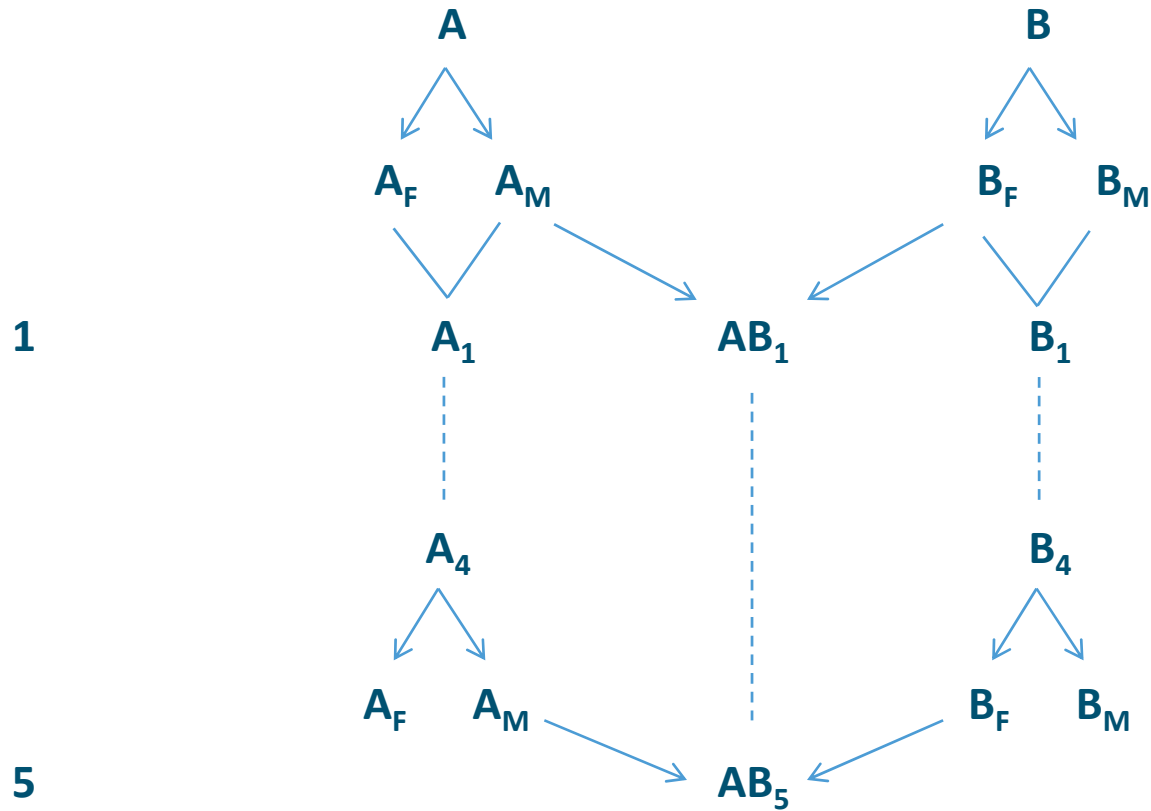
- To investigate the benefits of distinguishing two types of heterozygotes in crossbreds

SIMULATION STEPS



SIMULATION STEPS

Generations



SIMULATION PARAMETERS

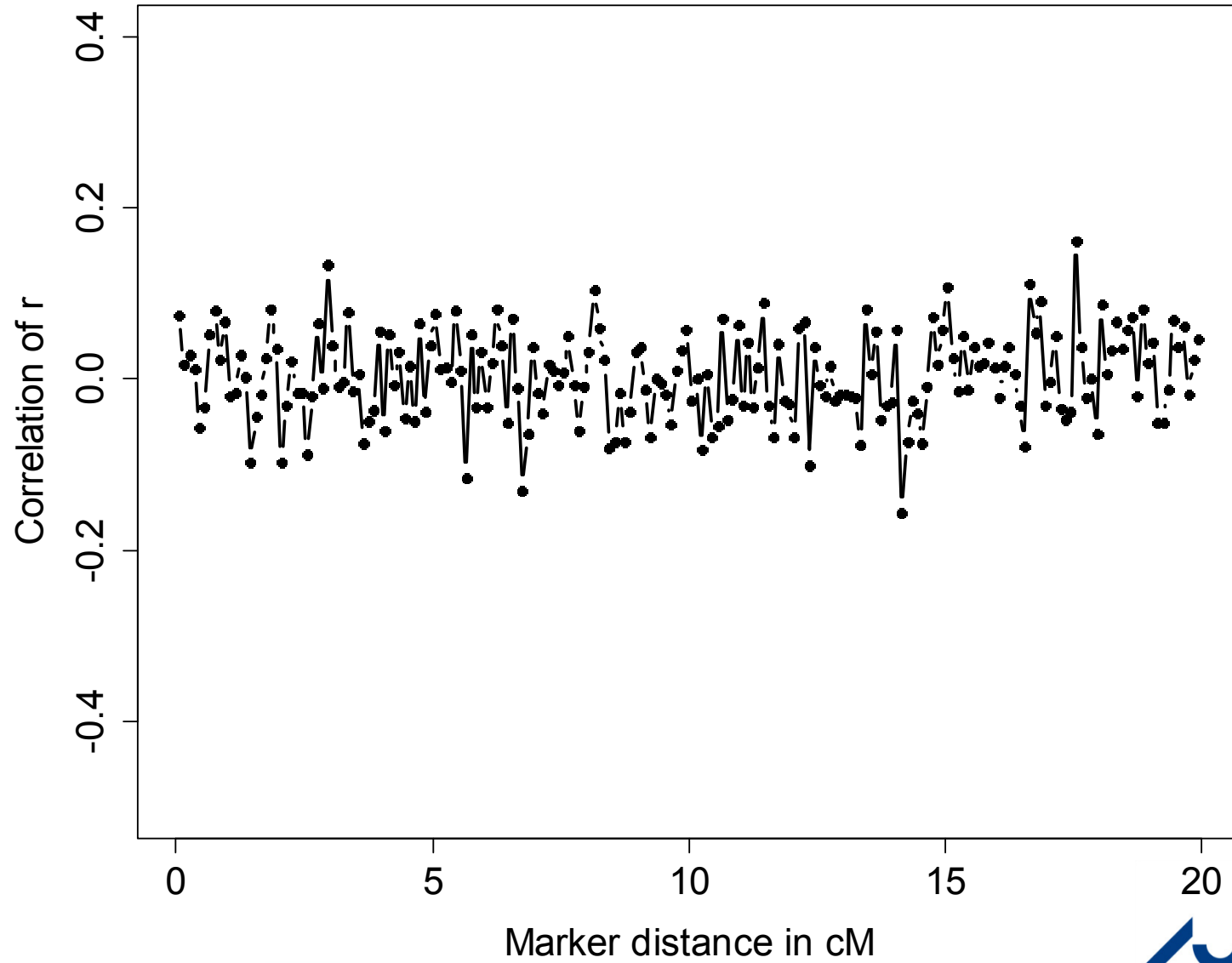
Number of chromosomes	1
Genome size	100 cM
Number of markers	1000
Number of QTL	100
Additive effects for QTL	Gamma
Dominance degrees (h_i)	Normal
Dominance effects for QTL	$d_i = h_i \cdot a_i $
Heritability	0.4 (0.3,0.1)

SCENARIOS

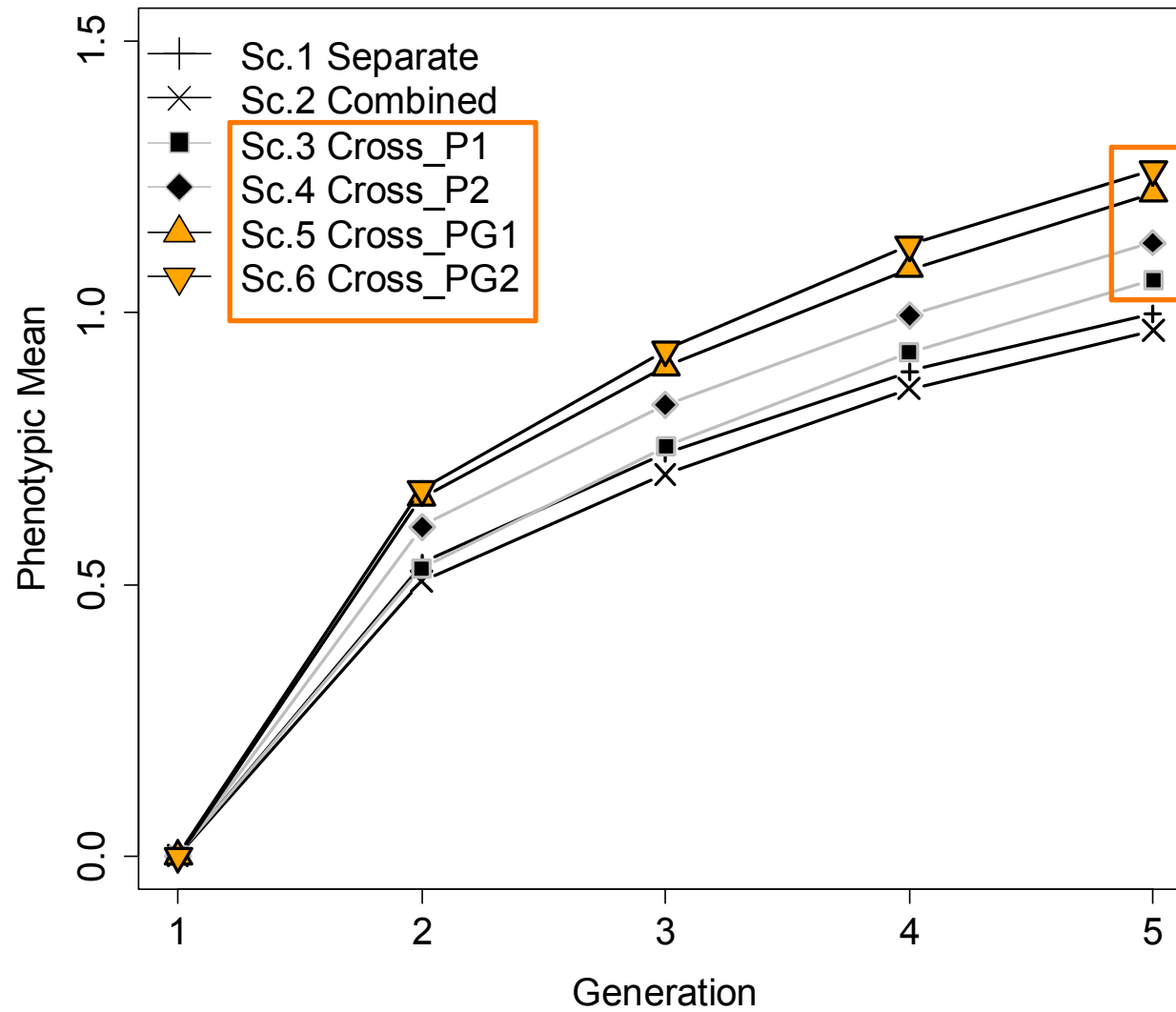
Scenarios	Training	
Sc. 1	Separate (A, B)	
Sc. 2	Combined (A+B)	
Sc. 3	Crossbreds (F ₁) P	
Sc. 4	Crossbreds (F ₁) P	M ₁ M ₂ /M ₂ M ₁
Sc. 5	Crossbreds (F ₁) P+G	
Sc. 6	Crossbreds (F ₁) P+G	M ₁ M ₂ /M ₂ M ₁

AA-Aa-aa
AA-Aa-aA-aa

CORRELATION OF PHASE

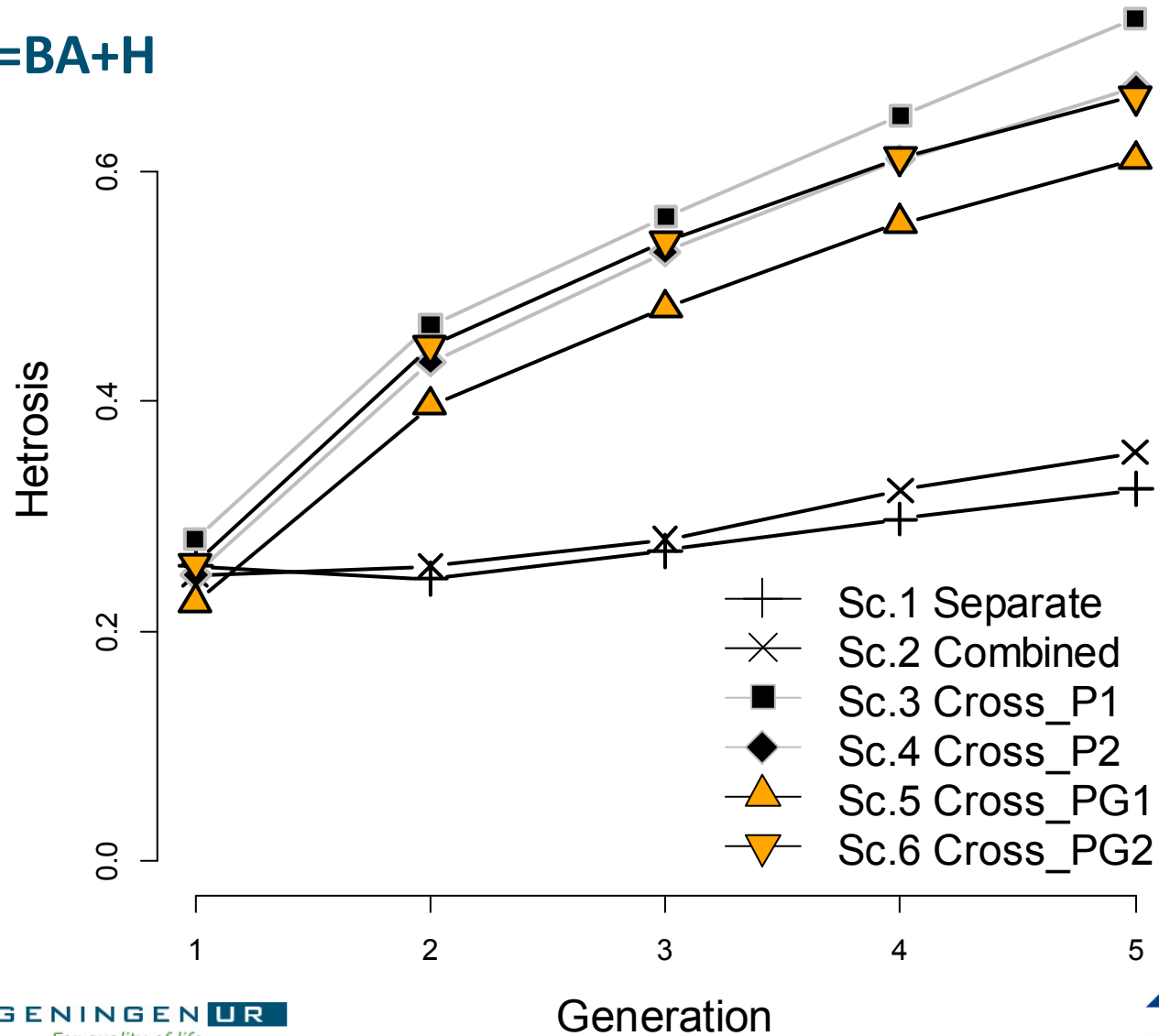


CUMULATIVE RESPONSE TO SELECTION IN CROSSBREDS



HETEROISIS

CP=BA+H



CONCLUSION

Thank YOU!

- Training on crossbred progeny gives higher response to selection than training on pure lines
- Distinguishing two types of heterozygotes would increase response to selection
- If correlation of phase between two breeds is low, joining breeds won't help

$$E(r) = r_0^2(1 - c)^{2T}$$

- r_0^2 is LD in the common ancestral population
- c is the recombination rate between markers
- T is the time since breed divergence in generations

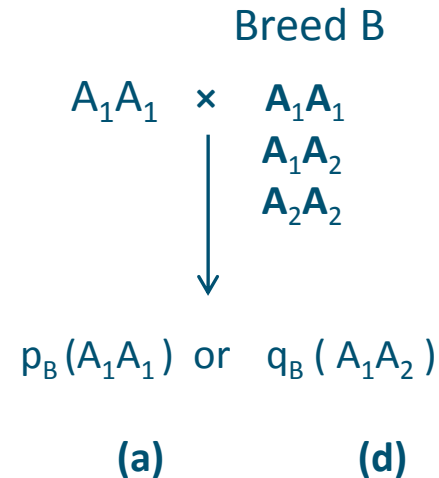
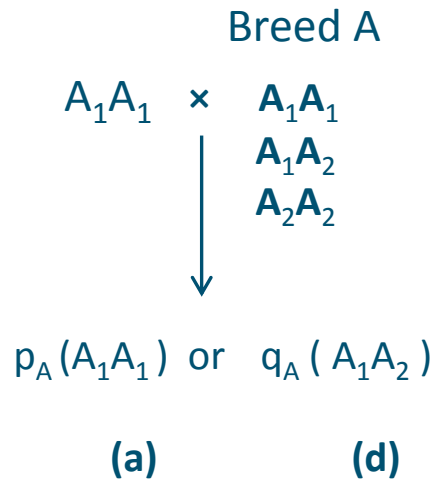
Selection criteria

GEBVP: Genomic Estimated Breeding value for PUREBRED

GEBVC: Genomic Estimated Breeding value for CROSSBRED

A_1A_2	
Breed A	Breed B
$p_A q_A$	$p_B q_B$

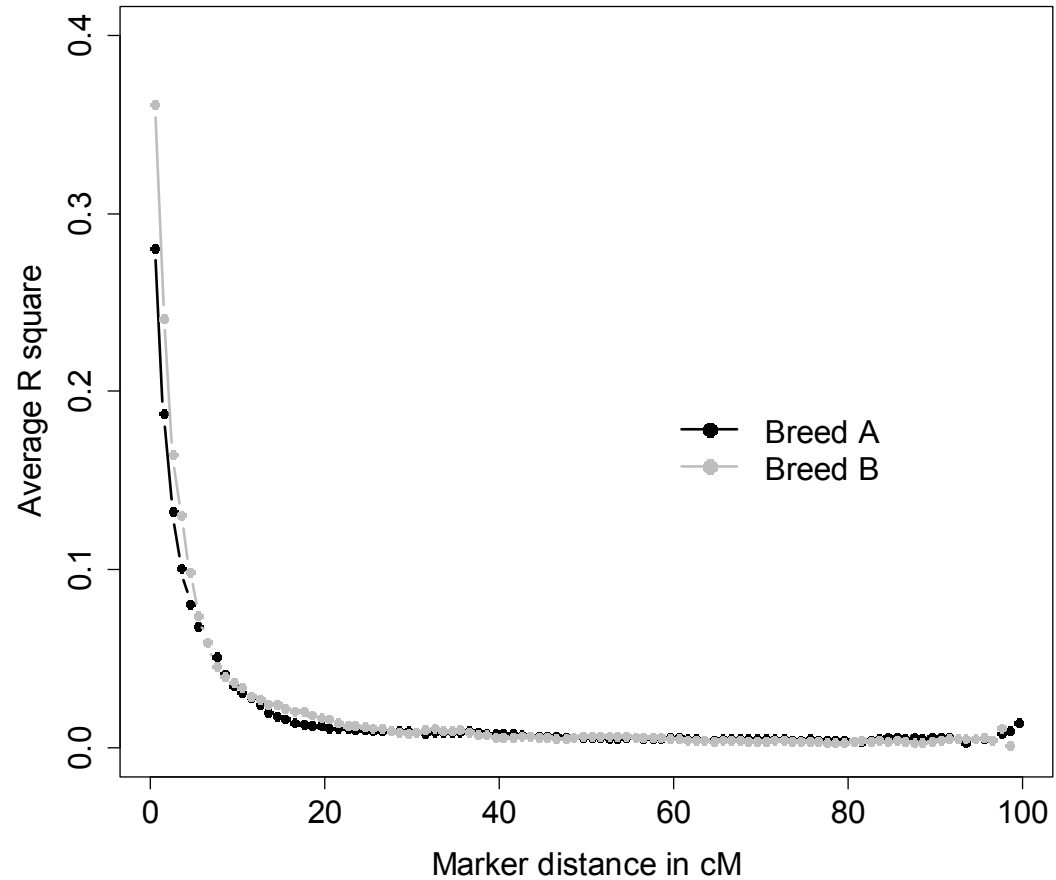
$$A_1A_1 \longrightarrow \begin{matrix} \text{GEBVP: } p_A \times a + q_A \times d \\ \text{GEBVC: } p_B \times a + q_B \times d \end{matrix}$$



Results

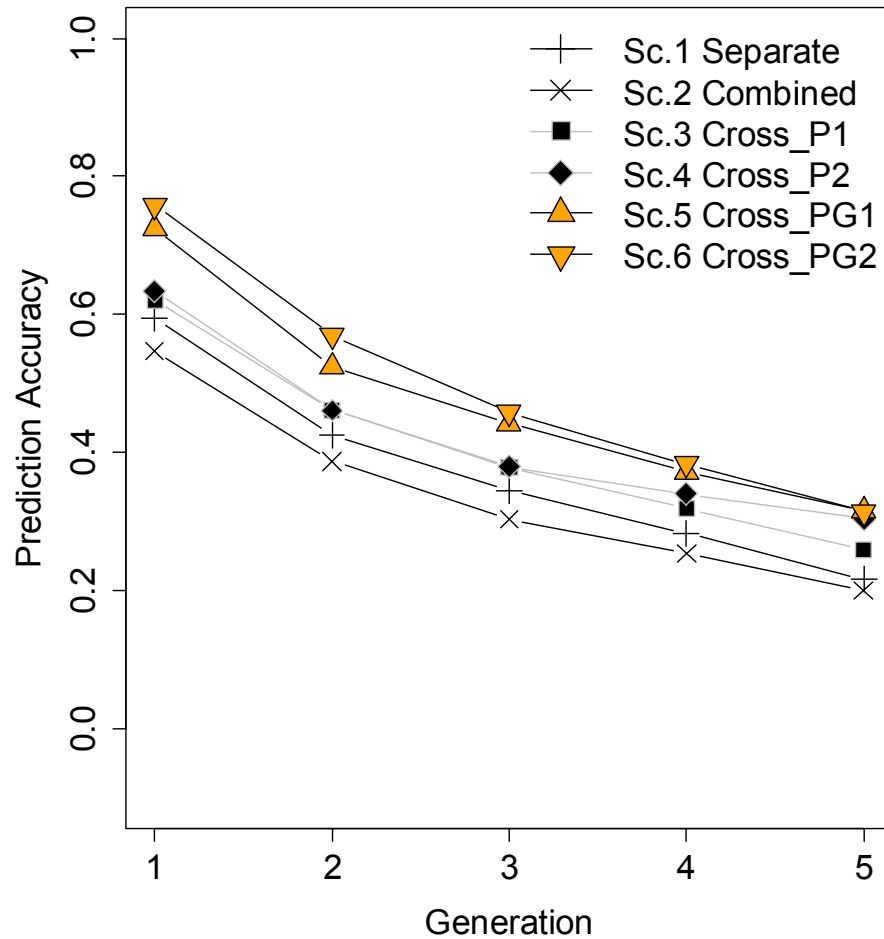
LD

Average $r^2 = 0.43$ Breed A
0.42 Breed B



PREDICTION ACCURACY

Accuracy of selection in Breed A



Accuracy of selection in Breed B

